

0590
12/13

#5

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/955,315

DATE: 12/11/2001

TIME: 15:48:51

Input Set : A:\032301.227.seq.ST25.txt

Output Set: N:\CRF3\12112001\I955315.raw

ENTERED

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3 <110> APPLICANT: Bathe, Brigitte
5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dps GENE
7 <130> FILE REFERENCE: 032301W227
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/955,315
C--> 9 <141> CURRENT FILING DATE: 2001-12-11
9 <160> NUMBER OF SEQ ID NOS: 4
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1377
15 <212> TYPE: DNA
16 <213> ORGANISM: Corynebacterium glutamicum
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (504)..(998)
21 <223> OTHER INFORMATION:
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27 tctccccgtc ggaaaggtgc aggcgaatct gccgcggggt ttcttcgcga ggttcaaact      120
29 gcaacgtgcc aatcagcccc aaatggatat acaaaatgtg ctcagggtga tccgcacga      180
31 actcgacgaa caggtgcttg ccgtaagcct ccgcaaccgc gatgcgggtga ccgttgatga      240
33 tcgccgcttc agaagtaaag cgtccttgag gtgaagtggc gtccaaaatg gtatcgccaa      300
35 aattcttggg gagttcccca gctagtogat gaatcacgtg tccttcaggc ataatcacca      360
37 accttagtag ccggtgtgcc gatttgataa aaaactaagc gtggcctgcg ggaatcggca      420
39 ctttcaggat aggacaacct aatataaata agcttaggct aagggccggg gacaatttat      480
41 caagcagtgc tataataggg gtc atg gca aac tac aca gtc cct gga atc aac      533
42                               Met Ala Asn Tyr Thr Val Pro Gly Ile Asn
43                               1           5           10
45 gag aat gac gca aag cag ctt att gat gga ctg cag gag cgt ctc acc      581
46 Glu Asn Asp Ala Lys Gln Leu Ile Asp Gly Leu Gln Glu Arg Leu Thr
47                               15           20           25
49 gac tac aac gat ctt cac ctc atc ttg aag cac gtg cac tgg aac gtc      629
50 Asp Tyr Asn Asp Leu His Leu Ile Leu Lys His Val His Trp Asn Val
51                               30           35           40
53 act ggc ccc aac ttc att gct gtt cac gaa atg ctc gac cca cag gtt      677
54 Thr Gly Pro Asn Phe Ile Ala Val His Glu Met Leu Asp Pro Gln Val
55                               45           50           55
57 gac ctt gtt cgt ggc tat gct gac gaa gtt gca gag cgc att tcc acc      725
58 Asp Leu Val Arg Gly Tyr Ala Asp Glu Val Ala Glu Arg Ile Ser Thr
59                               60           65           70
61 ctc gga ggc gca cca gtt gga acc cca gaa ggc cac gtt gct gac cgc      773
62 Leu Gly Gly Ala Pro Val Gly Thr Pro Glu Gly His Val Ala Asp Arg
63 75                               80           85           90
65 acc cca ctg caa tat gag cgc aat gcc gga aat gtc caa gca cac ctc      821
66 Thr Pro Leu Gln Tyr Glu Arg Asn Ala Gly Asn Val Gln Ala His Leu
67                               95           100          105
69 act gac ctc aat cgc gtg tac acc caa gtg ctg acc gga gtt cgc gag      869
70 Thr Asp Leu Asn Arg Val Tyr Thr Gln Val Leu Thr Gly Val Arg Glu

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71          110          115          120
73 tcc atg gca tca gcc ggc cca gtg gat cca gta act gaa gac atc tac      917
74 Ser Met Ala Ser Ala Gly Pro Val Asp Pro Val Thr Glu Asp Ile Tyr
75          125          130          135
77 atc agc cag gcc gcg gag ctg gag aaa ttc cag tgg ttc atc cgc gca      965
78 Ile Ser Gln Ala Ala Glu Leu Glu Lys Phe Gln Trp Phe Ile Arg Ala
79          140          145          150
81 cac att gtt gat gta gac gga aac atc caa gag taaaacgtcg aaaagcgtaa      1018
82 His Ile Val Asp Val Asp Gly Asn Ile Gln Glu
83 155          160          165
85 aggcgctgac cccaccagc ccgggggtca gtggcttcct tagtgcaaaa atccaccaca      1078
87 aaatttttga tcctgaaatt tgtgggtgat ttttgcactt ttcgtcgccg gatcctgcac      1138
89 gaatccacca cagactccgg aatttgccgt gggatgtggg ggatccttgc tgtggaacct      1198
91 cacaggaggt gcaagttggg ggacggagtg ttgggattgc taaaattcgt tcgattttta      1258
93 agttctccgc tgatctgtaa cgagaagtg aacagtcaac ctgcagtgac cccgcaggaa      1318
95 tcacagcagc ctcaatcgcc tcaaaagtaa cgctcctaga atcgctcta agggcctaa      1377
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99 <211> LENGTH: 165
100 <212> TYPE: PRT
101 <213> ORGANISM: Corynebacterium glutamicum
103 <400> SEQUENCE: 2
105 Met Ala Asn Tyr Thr Val Pro Gly Ile Asn Glu Asn Asp Ala Lys Gln
106 1          5          10          15
109 Leu Ile Asp Gly Leu Gln Glu Arg Leu Thr Asp Tyr Asn Asp Leu His
110          20          25          30
113 Leu Ile Leu Lys His Val His Trp Asn Val Thr Gly Pro Asn Phe Ile
114          35          40          45
117 Ala Val His Glu Met Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr
118          50          55          60
121 Ala Asp Glu Val Ala Glu Arg Ile Ser Thr Leu Gly Gly Ala Pro Val
122 65          70          75          80
125 Gly Thr Pro Glu Gly His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu
126          85          90          95
129 Arg Asn Ala Gly Asn Val Gln Ala His Leu Thr Asp Leu Asn Arg Val
130          100          105          110
133 Tyr Thr Gln Val Leu Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly
134          115          120          125
137 Pro Val Asp Pro Val Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu
138          130          135          140
141 Leu Glu Lys Phe Gln Trp Phe Ile Arg Ala His Ile Val Asp Val Asp
142 145          150          155          160
145 Gly Asn Ile Gln Glu
146          165
149 <210> SEQ ID NO: 3
150 <211> LENGTH: 28
151 <212> TYPE: DNA
152 <213> ORGANISM: Corynebacterium glutamicum
154 <400> SEQUENCE: 3
155 caggtaccat aagcttaggc taagggcc

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158 <210> SEQ ID NO: 4

159 <211> LENGTH: 28

160 <212> TYPE: DNA

161 <213> ORGANISM: Corynebacterium glutamicum

163 <400> SEQUENCE: 4

164 tgtctagagc actaaggaag ccactgac

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date